

FIGURE 1: ISS-pST gene construct

*From  
Amendment*

1 GCTAGCATGG CCCTGTGGAT GCGCCTCCTG CCCCTGCTGG CGCTGCTGGC  
5 51 CCTCTGGGGA CCTGACCCAG CCGCAGCCCT CGAGATGTTT CCAGCTATGC  
101 CACTTTCTTC TCTGTTGCT AACGCTGTTT TTCGGGCCCA GCACCTGCAC  
151 CAACTGGCTG CCGACACCTA CAAGGAGTTT GAGCGCGCCT ACATCCCGGA  
201 GGGACAGAGG TACTCCATCC AGAACGCCCA GGCTGCCTTC TGCTTCTCGG  
251 AGACCATCCC GGCCCCACG GGCAAGGACG AGGCCAGCA GAGATCGGAC  
10 301 GTGGAGCTGC TGCCTTCTC GCTGCTGCTC ATCCAGTCGT GGCTCGGGCC  
351 CGTGCACTTC CTCAGCAGGG TCTTACCAA CAGCCTGGTG TTTGGCACCT  
401 CAGACCGCGT CTACGAGAAG CTGAAGGACC TGGAGGAGGG CATCCAGGCC  
451 CTGATGCGGG AGCTGGAGGA TGGCAGCCCC CGGGCAGGAC AGATCCTCAA  
501 GCAAACCTAC GACAAATTTG ACACAACTT GCGCAGTGAT GACGCGCTGC  
15 551 TTAAGAACTA CGGGCTGCTC TCCTGCTTCA AGAAGGACCT GCACAAGGCT  
601 GAGACATACC TGCGGGTCAT GAAGTGTCGC CGCTTCGTGG AGAGCAGCTG  
651 TGCCTTCTAG TCTAGA (SEQ ID NO: 4)

20 ATG...GCC- insulin secretory signal.

GCTAGC- *Nhe* I restriction site incorporated into construct in order to ligate into plasmid.

CTCGAG- *Xho* I restriction site incorporated into construct in order to ligate secretory signal and pST.

25 TCTAGA- *Xba* I restriction site incorporated into construct in order to ligate into plasmid.

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**FIGURE 2: ISS-pST peptide sequence.**

1    MALWMRLPL LALLALWGPD PAAALEMFPA MPLSSLFANA VLRAQHLHQL  
5    51   AADTYKEFER AYIPEGQRYIS IQNAQAACF SETIPAPTGK DEAQQRSDVE  
101   LLRFSLLLIQ SWLGPVQFLS RVFTNSLVFG TSDRVYEKLE DLEEGIQALM  
151   RELEDGSPRA GQILKQTYDK FDTNLRSDDA LLKNYGLLSC FKKDLHKAET  
201   YLRVMKCRRE VESSCAF    (SEQ ID NO:3)

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MAL.....AAA- insulin secretory signal, cleaved upon secretion of pST.

LE- function of XhoI cleavage site; result in no predicted secondary structural changes to pST.